(FILE 'HOME' ENTERED AT 16:06:34 ON 08 FEB 2004)

FILE 'MEDLINE, EMBASE, BIOSIS' ENTERED AT 16:06:41 ON 08 FEB 2004

L1	72	S	MICROCON
L2	12	S	MICROCON AND (("DNA PURIFICATION") OR ("DNA ISOLATION"))
L3	8	DUP	REM L2 (4 DUPLICATES REMOVED)
L4	123866	S	(DNA OR RNA OR "NUCLEIC ACID")(P)(PRIMER OR PROBE)
L5	1783	S	L4 (P) BIOTIN
L6	1288	S	L5 (P) HYBRIDIZ?
L7	3	S	L6 (P) TRANSFORM
L8	450	S	"URACIL DNA GLYCOLASE" OR UDG
L9	0	S	L5 AND L8
L10	25	S	L4 AND L8
L11	13	DUP	REM L10 (12 DUPLICATES REMOVED)
L12	5	S	L11 NOT PY>=1994
L13	172	S	L5 AND "SINGLE STRANDED"
L14	101	DUP	REM L13 (71 DUPLICATES REMOVED)
L15	50	S	L14 NOT PY>=1994
L16	9	S	L15 AND TARGET
L17	110	S	L5 AND (SCREEN OR LIBRARY)
L18	49	DUP	REM L17 (61 DUPLICATES REMOVED)
L19	20	S	L18 NOT PY>=1994

3 ANSWER 2 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 2000:160165 BIOSIS
DOCUMENT NUMBER: PREV200000160165
TITLE: Extremely high levels of human mitochondrial DNA heteroplasmy in single hair roots.
AUTHOR(S): Grzybowski, Tomasz [Reprint author]
CORPORATE SOURCE: Forensic Medicine Institute, The Ludwik Rydygier University School of Medical Sciences, ul. M. Curie-Sktodowskiej 9, 85-094, Bydgoszcz, Poland
SOURCE: Electrophoresis, (Feb., 2000) Vol. 21, No. 3, pp. 548-553. print.
CODEN: ELCTDN. ISSN: 0173-0835.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 26 Apr 2000
Last Updated on STN: 4 Jan 2002

AB For many years it has been assumed that the vast majority of mitochondrial genomes of a single individual are identical, both in the same tissue and within different tissues. Incidences of heteroplasmy (i.e., the occurrence of two or more codominating types of molecules within the mitochondrial DNA population of the same individual) were thought to be extremely rare. This study strongly supports the thesis that heteroplasmy is a principle, rather than an exception, in mitochondrial DNA genetics. During direct sequencing of the first hypervariable segment of the human mitochondrial control region (HV1) in 100 single hair roots obtained from 35 individuals, 24 different heteroplasmic positions were identified. Unusually high levels of heteroplasmy (up to six positions in the HV1 region) were encountered in two individuals. Two individuals related in maternal lineage shared the same heteroplasmic positions. Moreover, highly variable levels of heteroplasmy were observed even among roots from the same individual. The most probable mechanisms involved in generating so many mismatches are mutations occurring presumably in the female germline, followed by differential segregation of mitotypes during the development of individual hairs. Generally, heteroplasmy complicates sequence comparisons in mitochondrial DNA testing performed for forensic purposes, but in some cases it can substantially increase the discriminating power of the analysis.

L3 ANSWER 3 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 2000:309010 BIOSIS
DOCUMENT NUMBER: PREV200000309010
TITLE: Genetic typing and HIV-1 diagnosis by using 96 capillary array electrophoresis and ultraviolet absorption detection.
AUTHOR(S): Gong, Xiaoyi; Yeung, Edward S. [Reprint author]
CORPORATE SOURCE: Ames Laboratory-USDOE and Department of Chemistry, Iowa State University, Ames, IA, 50011, USA
SOURCE: Journal of Chromatography B, (April 28, 2000) Vol. 471, No. 1, pp. 15-21. print.
CODEN: JCBADL. ISSN: 0378-4347.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 19 Jul 2000
Last Updated on STN: 7 Jan 2002

AB Current high-throughput approaches to the analysis of PCR products are based primarily on electrophoretic separation and laser-excited fluorescence detection. We show that capillary array electrophoresis can be applied to HIV-1 diagnosis and D1S80 VNTR genetic typing based simply on UV absorption detection. The additive contribution of each base pair to the total absorption signal provides adequate detection sensitivity for analyzing most PCR products. Not only is the use of specialized and potentially toxic fluorescent labels eliminated, but also the complexity and cost of the instrumentation are greatly reduced.

L3 ANSWER 4 OF 8 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN
ACCESSION NUMBER: 1999313131 EMBASE
TITLE: NaOH treatment to neutralize inhibitors of Taq polymerase.
AUTHOR: Bourke M.T.; Scherczinger C.A.; Ladd C.; Lee H.C.
CORPORATE SOURCE: Dr. M.T. Bourke, C.S.P. Forensic Science Laboratory, 278 Colony St, Meriden, CT 06451, United States
SOURCE: Journal of Forensic Sciences, (1999) 44/5 (1046-1050). Refs: 11
ISSN: 0022-1198 CODEN: JFSCAS
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
049 Forensic Science Abstracts
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The introduction of polymerase chain reaction (PCR) into the forensic field has greatly extended the ability to analyze DNA from small or degraded samples. However, one significant problem with PCR analysis is the sensitivity of Taq Polymerase to inhibitors found in many substrates commonly encountered with evidentiary materials. We hypothesize that the most problematic of these compounds intercalate into double stranded DNA (dsDNA) and have significantly less affinity for single stranded DNA (ssDNA). This study presents a comprehensive analysis of a novel method for the neutralization of Taq inhibitors by denaturation and washing with NaOH in **Microcon**-100 filtration units. The data show that DNA recovered following NaOH repurification routinely amplifies when other inhibitor neutralization techniques are unsuccessful. Genetic profiles have been obtained with both AmpliType PM + DQA1 and D1S80 systems. However, the NaOH protocol is not advised when the quantity of DNA is limited since the treatment results in significant loss of DNA.

L3 ANSWER 5 OF 8 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 1998248731 MEDLINE
DOCUMENT NUMBER: 98248731 PubMed ID: 9587179
TITLE: Use of **DNA purification** kits for polymerase chain reaction testing of Gen-Probe Chlamydia trachomatis PACE 2 specimens.
AUTHOR: Gossack J P; Beebe J L
CORPORATE SOURCE: Laboratory and Radiation Services Division, Colorado Department of Public Health and Environment, Denver, USA.. beebe@state.co.us
SOURCE: SEXUALLY TRANSMITTED DISEASES, (1998 May) 25 (5) 265-71. Journal code: 7705941. ISSN: 0148-5717.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199807
ENTRY DATE: Entered STN: 19980716
Last Updated on STN: 19980716
Entered Medline: 19980709
AB BACKGROUND AND OBJECTIVES: Confirmation testing using nucleic acid amplification has been shown to improve the sensitivity and specificity of screening tests for Chlamydia trachomatis. However, no critical information on the use of these techniques as an adjunct to Gen-Probe hybridization testing, one of the most common screening methods, has been reported to date. We examined the Roche AMPLICOR PCR C. trachomatis Test (Roche Diagnostic Systems, Branchburg, NJ) as a confirmatory test for the Gen-Probe PACE 2 C. trachomatis Test (San Diego, CA). Further, to mitigate the possible effect of interfering compounds in the Gen-Probe PACE 2 transport medium, we tested various **DNA purification** techniques. STUDY DESIGN: C. trachomatis elementary

bodies were used to spike PACE 2 Transport medium, which was serially diluted, then tested by polymerase chain reaction (PCR). Six parallel dilution series were conducted: (1) saline dilutions tested by the Syva Direct Specimen Test, (2) Roche AMPLICOR transport medium dilutions tested by PCR, and (3-6) dilutions in PACE 2 transport medium purified respectively by GENECLEAN II (BIO101, Vista, CA), Puregene (Gentra Systems, Inc., Research Triangle Park, NC), **Microcon** 100 (Amicon, Inc., Beverly, MA) **DNA isolation** kits, and no **DNA purification**, all tested by PCR. The system giving the best results by in vitro endpoint dilution trials was then used to confirm human specimens previously tested by the Gen-Probe method. RESULTS: PCR detected C. trachomatis at 11 twofold dilutions greater than PACE 2 and equivalent to detection of single elementary body by Syva Direct Specimen Test. **DNA purification** of spiked PACE 2 transport medium by the **Microcon** 100 kit produced the most consistent PCR detection endpoints, equivalent to endpoints of spiked AMPLICOR transport medium. Endpoints with no **DNA purification** step were variable and lower. Of 78 endocervical specimens negative by PACE 2 and Gen-Probe Probe Competition Assay, 12 (15.3%) were positive by **Microcon DNA purification**/PCR testing. CONCLUSIONS: PCR can be used as confirmation method for Gen-Probe PACE 2 testing, but testing must be performed with a **DNA purification** procedure.

L3 ANSWER 6 OF 8 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 1998024546 EMBASE
TITLE: Methods for extracting and amplifying genomic DNA isolated from frozen serum.
AUTHOR: Dixon S.C.; Horti J.; Guo Y.; Reed E.; Figg W.D.
CORPORATE SOURCE: W.D. Figg, National Cancer Institute, National Institutes of Health, Building 10, 9000 Rockville Pike, Bethesda, MD 20892, United States. wdfigg@helix.nih.gov
SOURCE: Nature Biotechnology, (1998) 16/1 (91-94).
Refs: 14
ISSN: 1087-0156 CODEN: NABIF
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 029 Clinical Biochemistry
LANGUAGE: English

L3 ANSWER 7 OF 8 MEDLINE on STN DUPLICATE 2

ACCESSION NUMBER: 97449822 MEDLINE
DOCUMENT NUMBER: 97449822 PubMed ID: 9304838
TITLE: DNA extraction from liquid blood using QIAamp.
AUTHOR: Scherczinger C A; Bourke M T; Ladd C; Lee H C
CORPORATE SOURCE: Connecticut State Police Forensic Science Laboratory, Meriden, USA.
SOURCE: JOURNAL OF FORENSIC SCIENCES, (1997 Sep) 42 (5) 893-6.
Journal code: 0375370. ISSN: 0022-1198.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199710
ENTRY DATE: Entered STN: 19971224
Last Updated on STN: 19971224
Entered Medline: 19971028

AB The implementation of convicted felon DNA databases by increasing numbers of forensic science laboratories has engendered the need for a quick, efficient, and cost-effective method for the isolation of DNA from liquid blood samples. Because of the large numbers of samples involved, the ideal method would combine high throughput capability with maximal yield,

high quality, and minimal time. We have found that the QIAGEN QIAamp Blood Kit/Tissue Kit satisfy all of these requirements. This simple, low cost spin column procedure yields purified DNA of approximately 20-30 kb that can be used directly in PCR or other enzymatic reactions without further purification. We compared the QIAamp isolation procedure to the standard SDS-Proteinase K/organic extraction/**microcon** purification procedure currently used by many forensic laboratories. The QIAamp procedure consistently gave a two- to four-fold increased yield relative to the organic extraction procedure. The DNA obtained was of high molecular weight, exhibited little degradation, and was suitable for RFLP and PCR analyses. We have found QIAGEN's QIAamp **DNA isolation** procedure to be ideally suited for preparation of samples for DNA databasing.

L3 ANSWER 8 OF 8 EMBASE
on STN

ACCESSION NUMBER: 95105032 EMBASE
DOCUMENT NUMBER: 1995105032
TITLE: Recovery of DNA, RNA and protein from gels with microconcentrators.
AUTHOR: Krowczynska A.M.; Donoghue K.; Hughes L.
CORPORATE SOURCE: Amicon, Inc., 72 Cherry Hill Drive,Beverly, MA 01915-1065, United States
SOURCE: BioTechniques, (1995) 18/4 (698-703).
ISSN: 0736-6205 CODEN: BTNQDO
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 027 Biophysics, Bioengineering and Medical Instrumentation
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The use of a new product, **Microcon**.RTM./Micropure(TM) (a centrifugal ultrafiltration device combined with a microporus insert), for the purification of DNA, RNA, peptides and proteins from gels is described. Using this system, DNA can be recovered from agarose gel in concentrated, contamination-free form in only 15 min. Results of studies on the effects of fragment size and various pretreatment of the gel slice on DNA recovery are presented. The **Microcon**/Micropure combination can also be used for the recovery of macromolecules from polyacrylamide gels. Optimized protocols for the recovery of RNA, oligonucleotides and proteins from polyacrylamide gels using a crush and elute method, along with a study of critical parameters, are presented.